Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION** **SERIAL NUMBER:** 09/914,006C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
4	Non-ASCII	The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
5	Variable Length	Sequence(s)____contain n's or.Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence. <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial *anything*, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or contains Artificial.
11	Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response contains the word "Artificial" or "Unknown." Please explain source of genetic material in <220> to <223> section, i.e., why you chose Artificial or Unknown. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12	PatentIn "bug"	Please do not use "Copy to Disk" function of PatentIn. In PatentIn 2.x it causes a corrupted file and in PatentIn 3.x you may lose your hard returns in the sequence listing. Instead, please use "Windows Explorer" or any other manual means to copy file to floppy disk.

PCT

RAW SEQUENCE LISTING DATE: 01/22/2003
PATENT APPLICATION: **US/09/914,006C** TIME: 13:42:48

Input Set : **A:\SN09914006.asc**
Output Set: **N:\CRF4\01222003\I914006C.raw**

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  3 <110> APPLICANT: Eggeling, Lothar
  4       Sahm, Hermann
  6 <120> TITLE OF INVENTION: METHOD FOR MICROBIALLY PRODUCING L-VALINE
  8 <130> FILE REFERENCE: 5899*13
 10 <140> CURRENT APPLICATION NUMBER: 09/914006C
C--> 11 <141> CURRENT FILING DATE: 2002-11-07
 13 <150> PRIOR APPLICATION NUMBER: PCT/EP00/01405
 14 <151> PRIOR FILING DATE: 2000-02-21
 16 <160> NUMBER OF SEQ ID NOS: 7
 18 <170> SOFTWARE: PatentIn version 3.1
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ERRORED SEQUENCES

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 21 <211> LENGTH: 2952
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Corynebacterium glutamicum
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 27 gatgacgaca    60
E--> 29 ccgatgggaa tacaacacaa acagaaagcg ttgaatccca agagaccgga
 30 caagccgcgt   120
E--> 32 ctgaaacctc acatcgtgat aaccctgcgt cacagcacta gagtgtaata
 33 agccgtccga   180
E--> 35 accaaaggtc cacacctctg cacgagtaga agctcaccca agttttcaaa
 36 gtgccgttga   240
E--> 38 ttcttgacaa ccacccgccg ctctttagag cagatttgaa aagcgcatca
 39 tgatcccact   300
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 42 tttggcgtgc   360
E--> 44 caccggcacc aaggaaaatg agttcggcaa gccaattgtt gccatcgtaa
 45 actcctacac   420
E--> 47 ccagttcgtg ccccgacacg ttcaccttaa gaacgtcggc gatattgtgg
 48 cagatgcagt   480
E--> 50 gcgcaaagcc ggtggcgttc caaaggaatt caacaccatc gtcgatgacg
 51 gcatcgccat   540
E--> 53 gggacacggc ggcatgctgt actccctgcc atcccgtgaa atcatcgccg
 54 actccgtcga   600
E--> 56 atacatggtc aacgcacaca ccgccgacgc catggtgtgt atctccaact
 57 gtgacaagat   660
E--> 59 cacccccaggc atgctcaacg cagcaatgcg cctgaacatc ccagtggtct
 60 tcgtttccgg   720
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move wrapped sequences & numbering back to previous Line, See Item # 1 on ERROR Summary SHEET and 37CFR 1.822 (e)

RAW SEQUENCE LISTING DATE: 01/22/2003
PATENT APPLICATION: US/09/914,006C TIME: 13:42:48

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Output Set: N:\CRF4\01222003\I914006C.raw

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63 caccaaccga 780
E--> 65 cctcatcacc gcgatctccg catccgcaag cgatgcagtc gacgacgcag
66 gccttgcagc 840
E--> 68 cgttgaacga tccgcatgcc caacctgtgg ctcctgctcc ggtatgttca
69 ccgcgaactc 900
E--> 71 catgaactgc ctcacccgaag ctctgggact ttctctcccg ggcaacggct
72 ccactctggc 960
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75 ttgaactgtg 1020
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78 ccaccaagaa 1080
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81 acaccatcct 1140
E--> 83 ccacatcctc gcagctgccc aggaaggcga agttgacttc gacctcgcag
84 acatcgacga 1200
E--> 86 actgtccaaa aacgtcccct gcctgtccaa ggttgcacca aactccgact
87 accacatgga 1260
E--> 89 agacgtccac cgcgccggtc gcattccagc actgctcggc gagctcaacc
90 gcggtggcct 1320
E--> 92 gctgaacaag gacgtccact ccgttcactc caacgacctt gaaggttggt
93 tggatgactg 1380
E--> 95 ggatatccgc tctggcaaga ccaccgaagt agcaaccgaa ctcttccacg
96 cagccccagg 1440
E--> 98 tggcatccgc accaccgaag cattctccac cgagaaccgc tgggacgaac
99 tcgacaccga 1500
E--> 101 cgctgccaag ggctgcatcc gcgacgttga acacgcctac accgccgacg
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105 gtatcgaaga 1620
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E--> 110 tgtcatcctg accaagacca tccaagctgg cgaagttctg gtcgtccgct
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E--> 113 atcaggtgga ccaggcatgc aggaaatgct tcacccaacc gcattcctca
114 agggatccgg 1800
E--> 116 cctgggcaag aagtgtgcac tgatcaccga cggccgtttc tccggaggtt
117 cctcaggact 1860
E--> 119 gtccatcggc cacgtctccc cagaagcagc acacggcgga gtcattggtc
120 tgatcgaaaa 1920
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129 cctccgctga 2100
E--> 131 taagggtgca gtccgtcagg tcgactaacc ctttgtgagt gtttgagcac
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E--> 134 ctttgggttc cggtgctttt tcatgtcttg gcctgtgtgg gcgtggtgga

same as page 1

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Input Set : **A:\SN09914006.asc**
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E--> 137 gcaaatactc accacaagtt gcaggatttc tgctggttgt ggtggatttt
     138 cccgctttat   2280
E--> 140 agccctatgc gtgcaacttt cggaccgatt ccaaagggca aagccctgtt
     141 tgtggtggat   2340
E--> 143 ccttgccctg gaagctttca ggaaccacaa ctaccccact gaccccaaag
     144 tggataggcc   2400
E--> 146 ctattcttcc gtttaagcgc ctcaaacacc tctccccaca cttgacccat
     147 taggcaatta   2460
E--> 149 cgaatcctta aacagccttc tacagcacca tgccccaaac cgaacccagg
     150 catgaaaaag   2520
E--> 152 accctcacca ggagggtctt tttctaaaac tttggctacg cgattgggtt
     153 cacacccgca   2580
E--> 155 ccgaaccacc acagcagaac tgccgctgcg atgccgatga ccacgaagat
     156 ccacgagctc   2640
E--> 158 accagtggac gctttgccca acctcggcca gagtcaaggg aaatcttgcc
     159 ggggccggtg   2700
E--> 161 aactgaagtc cgacaaccac gatagtgagg atcagtgcca gcatcaatgg
     162 ctcactaagt   2760
E--> 164 tcaccccaac caccttcatg agtgttgact tggtgaaggg tggtaaagga
     165 tgtcgccacc   2820
E--> 167 gtggctaccg ctgctgccac tggggtcatc agaccaagga gcaggaagac
     168 accagccgca   2880
E--> 170 agttcaatag atggaagcag gatcgcgagg atttcaggcc actggtaacc
     171 agcgaactct   2940
E--> 173 gcctcgactc ta
     174 2952
     177 <210> SEQ ID NO: 2
     178 <211> LENGTH: 612
     179 <212> TYPE: PRT
     180 <213> ORGANISM: Corynebacterium glutamicum
     182 <400> SEQUENCE: 2
     184 Met Ile Pro Leu Arg Ser Lys Val Thr Thr Val Gly Arg Asn Ala
E--> 185 Ala
E--> 186 1               5                   10                  15
     189 Gly Ala Arg Ala Leu Trp Arg Ala Thr Gly Thr Lys Glu Asn Glu
E--> 190 Phe
E--> 191             20                  25                  30
     194 Gly Lys Pro Ile Val Ala Ile Val Asn Ser Tyr Thr Gln Phe Val
E--> 195 Pro
E--> 196         35                  40                  45
     199 Gly His Val His Leu Lys Asn Val Gly Asp Ile Val Ala Asp Ala
E--> 200 Val
E--> 201     50                  55                  60
     204 Arg Lys Ala Gly Gly Val Pro Lys Glu Phe Asn Thr Ile Val Asp
E--> 205 Asp
E--> 206 65                  70                  75                  80
     209 Gly Ile Ala Met Gly His Gly Gly Met Leu Tyr Ser Leu Pro Ser
E--> 210 Arg
```

Same as page 1

Same as page 1

RAW SEQUENCE LISTING DATE: 01/22/2003
PATENT APPLICATION: US/09/914,006C TIME: 13:42:48

Input Set : A:\SN09914006.asc
Output Set: N:\CRF4\01222003\I914006C.raw

Same as page 1

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E--> 211                    85                  90                  95
     214 Glu Ile Ile Ala Asp Ser Val Glu Tyr Met Val Asn Ala His Thr
E--> 215 Ala
E--> 216                100                 105                 110
     219 Asp Ala Met Val Cys Ile Ser Asn Cys Asp Lys Ile Thr Pro Gly
E--> 220 Met
E--> 221         115                 120                 125
     224 Leu Asn Ala Ala Met Arg Leu Asn Ile Pro Val Val Phe Val Ser
E--> 225 Gly
E--> 226     130                 135                 140
     229 Gly Pro Met Glu Ala Gly Lys Ala Val Val Val Glu Arg Val Ala
E--> 230 His
E--> 231 145                 150                 155
E--> 232 160
     235 Ala Pro Thr Asp Leu Ile Thr Ala Ile Ser Ala Ser Ala Ser Asp
E--> 236 Ala
E--> 237                165                 170                 175
     240 Val Asp Asp Ala Gly Leu Ala Ala Val Glu Arg Ser Ala Cys Pro
E--> 241 Thr
E--> 242                180                 185                 190
     245 Cys Gly Ser Cys Ser Gly Met Phe Thr Ala Asn Ser Met Asn Cys
E--> 246 Leu
E--> 247         195                 200                 205
     250 Thr Glu Ala Leu Gly Leu Ser Leu Pro Gly Asn Gly Ser Thr Leu
E--> 251 Ala
E--> 252     210                 215                 220
     255 Thr His Ala Ala Arg Arg Ala Leu Phe Glu Lys Ala Gly Glu Thr
E--> 256 Val
E--> 257 225                 230                 235
E--> 258 240
     261 Val Glu Leu Cys Arg Arg Tyr Tyr Gly Glu Glu Asp Glu Ser Val
E--> 262 Leu
E--> 263                245                 250                 255
     266 Pro Arg Gly Ile Ala Thr Lys Lys Ala Phe Glu Asn Ala Met Ala
E--> 267 Leu
E--> 268                260                 265                 270
     271 Asp Met Ala Met Gly Gly Ser Thr Asn Thr Ile Leu His Ile Leu
E--> 272 Ala
E--> 273         275                 280                 285
     276 Ala Ala Gln Glu Gly Glu Val Asp Phe Asp Leu Ala Asp Ile Asp
E--> 277 Glu
E--> 278     290                 295                 300
     281 Leu Ser Lys Asn Val Pro Cys Leu Ser Lys Val Ala Pro Asn Ser
E--> 282 Asp
E--> 283 305                 310                 315
E--> 284 320
     287 Tyr His Met Glu Asp Val His Arg Ala Gly Arg Ile Pro Ala Leu
E--> 288 Leu
E--> 289                325                 330                 335
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RAW SEQUENCE LISTING DATE: 01/22/2003
PATENT APPLICATION: US/09/914,006C TIME: 13:42:48

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     292 Gly Glu Leu Asn Arg Gly Gly Leu Leu Asn Lys Asp Val His Ser
E--> 293 Val
E--> 294             340                 345                 350
     297 His Ser Asn Asp Leu Glu Gly Trp Leu Asp Asp Trp Asp Ile Arg
E--> 298 Ser
E--> 299         355                 360                 365
     302 Gly Lys Thr Thr Glu Val Ala Thr Glu Leu Phe His Ala Ala Pro
E--> 303 Gly
E--> 304     370                 375                 380
     307 Gly Ile Arg Thr Thr Glu Ala Phe Ser Thr Glu Asn Arg Trp Asp
E--> 308 Glu
E--> 309 385                 390                 395
E--> 310 400
     313 Leu Asp Thr Asp Ala Ala Lys Gly Cys Ile Arg Asp Val Glu His
E--> 314 Ala
E--> 315             405                 410                 415
     318 Tyr Thr Ala Asp Gly Gly Leu Val Val Leu Arg Gly Asn Ile Ser
E--> 319 Pro
E--> 320             420                 425                 430
     323 Asp Gly Ala Val Ile Lys Ser Ala Gly Ile Glu Glu Glu Leu Trp
E--> 324 Asn
E--> 325         435                 440                 445
     328 Phe Thr Gly Pro Ala Arg Val Val Glu Ser Gln Glu Glu Ala Val
E--> 329 Ser
E--> 330     450                 455                 460
     333 Val Ile Leu Thr Lys Thr Ile Gln Ala Gly Glu Val Leu Val Val
E--> 334 Arg
E--> 335 465                 470                 475
E--> 336 480
     339 Tyr Glu Gly Pro Ser Gly Gly Pro Gly Met Gln Glu Met Leu His
E--> 340 Pro
E--> 341             485                 490                 495
     344 Thr Ala Phe Leu Lys Gly Ser Gly Leu Gly Lys Lys Cys Ala Leu
E--> 345 Ile
E--> 346             500                 505                 510
     349 Thr Asp Gly Arg Phe Ser Gly Gly Ser Ser Gly Leu Ser Ile Gly
E--> 350 His
E--> 351         515                 520                 525
     354 Val Ser Pro Glu Ala Ala His Gly Gly Val Ile Gly Leu Ile Glu
E--> 355 Asn
E--> 356     530                 535                 540
     359 Gly Asp Ile Val Ser Ile Asp Val His Asn Arg Lys Leu Glu Val
E--> 360 Gln
E--> 361 545                 550                 555
E--> 362 560
     365 Val Ser Asp Glu Glu Leu Gln Arg Arg Arg Asp Ala Met Asn Ala
E--> 366 Ser
E--> 367             565                 570                 575
     370 Glu Lys Pro Trp Gln Pro Val Asn Arg Asn Arg Val Val Thr Lys
```

Same as page 1

RAW SEQUENCE LISTING DATE: 01/22/2003
PATENT APPLICATION: US/09/914,006C TIME: 13:42:48

Input Set : A:\SN09914006.asc
Output Set: N:\CRF4\01222003\I914006C.raw

E--> 371 Ala Same as page 1
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375 Leu Arg Ala Tyr Ala Lys Met Ala Thr Ser Ala Asp Lys Gly Ala
E--> 376 Val
E--> 377 595 600 605
380 Arg Gln Val Asp
E--> 381 610
384 <210> SEQ ID NO: 3
385 <211> LENGTH: 2164
386 <212> TYPE: DNA
387 <213> ORGANISM: Corynebacterium glutamicum
389 <400> SEQUENCE: 3
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394 agtttcttaa 120
E--> 396 agtttctaag gcaactgcaa cgaggtattt tagaactctc cgagaaatgg
397 aattagttca 180
E--> 399 cgaggtcagc aaacgccctt tgcggtttgc gctcacggat aaaggtcgtg
400 agatagtagg 240 Same as page 1
E--> 402 tcttgaggta aaaatttgac tccataacga gaacttaatc gagcaacacc
403 cctgaacagt 300
E--> 405 gaatcaaatc ggaatttatt tattctgagc tggtcatcac atctatactc
406 atgcccatgt 360
E--> 408 caggcattga tgcaaagaaa atccgcaccc gtcatttccg cgaagctaaa
409 gtaaacggcc 420
E--> 411 agaaagtttc ggttctcacc agctatgatg cgctttcggc gcgcattttt
412 gatgaggctg 480
E--> 414 gcgtcgatat gctccttgtt ggtgattccg ctgccaacgt tgtgctgggt
415 cgcgatacca 540
E--> 417 ccttgtcgat caccttggat gagatgattg tgctggccaa ggcggtgacg
418 atcgctacga 600
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421 ccaaatcagg 660
E--> 423 cggtggagtc cgcgatccgg gtcatgcgtg aaacgggtgc ggctgcggtg
424 aagatcgagg 720
E--> 426 gtggcgtgga gatcgcgcag acgattcgac gcattgttga tgctggaatt
427 ccggttgtcg 780
E--> 429 gccacatcgg gtacaccccg cagtccgagc attccttggg cggccacgtg
430 gttcagggtc 840
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433 gcgggtgcgt 900
E--> 435 ttgcggttgt gttggagatg gttccagcag aggcagcgcg cgaggttacc
436 gaggatcttt 960
E--> 438 ccatcaccac tatcggaatc ggtgccggca atggcacaga tgggcaggtt
439 ttggtgtggc 1020
E--> 441 aggatgcctt cggcctcaac cgcggcaaga agccacgctt cgtccgcgag
442 tacgccacct 1080
E--> 444 tgggcgattc cttgcacgac gccgcgcagg cctacatcgc cgatatccac

RAW SEQUENCE LISTING DATE: 01/22/2003
PATENT APPLICATION: US/09/914,006C TIME: 13:42:48

Input Set : A:\SN09914006.asc
Output Set: N:\CRF4\01222003\I914006C.raw

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     448 cgcttatcga  1200
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     451 tacacagcgg  1260
E--> 453 acacgcctcg ttggttaaag cagcacgcgc tgaaaacgac actgttgtag
     454 ccagtatttt  1320
E--> 456 tgtcaatccc ctgcagtttg aagcactcgg tgattgcgat gattaccgca
     457 actatccccg  1380
E--> 459 ccaactcgac gccgatttag cactgcttga agaggcaggt gtggatattg
     460 tgttcgcacc  1440
E--> 462 cgatgtggag gaaatgtacc ccggtggctt gccactagtg tgggcgcgca
     463 ccggttccat  1500
E--> 465 cggaacaaaa ttggagggtg ccagcaggcc tggccatttc gatggtgtgg
     466 ctaccgtggt  1560
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     469 aagatgctca  1620
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     472 agattcgtcc  1680
E--> 474 cgttccgatt attcgtggcg ccgatggctt agccgaatcc agccgcaatc
     475 aacgtctttc  1740
E--> 477 tgcggatcag cgagcgcaag ctctggtgct gccgcaggtg ttgagtgggt
     478 tgcagcgtcg  1800
E--> 480 aaaagcagct ggtgaagcgc tagatatcca aggtgcgcgc gacaccttgg
     481 ccagcgccga  1860
E--> 483 cggcgtgcgc ttggatcacc tggaaattgt cgatccagcc accctcgaac
     484 cattagaaat  1920
E--> 486 cgacggcctg ctcacccaac cagcgttggt ggtcggcgcg attttcgtgg
     487 ggccggtgcg  1980
E--> 489 gttgatcgac aatatcgagc tctagtacca accctgcgtt gcagcacgca
     490 gcttcgcata  2040
E--> 492 acgcgtgctc agctcagtgt ttttaggtgc gcggtgcgga tcggaaccgg
     493 gagttggcca  2100
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E--> 498 caca
     499 2164
     502 <210> SEQ ID NO: 4
     503 <211> LENGTH: 271
     504 <212> TYPE: PRT
     505 <213> ORGANISM: Corynebacterium glutamicum
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E--> 510 Phe
E--> 511 1               5                   10                  15
     514 Arg Glu Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser
E--> 515 Tyr
E--> 516             20                  25                  30
     519 Asp Ala Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met
```

Same as page 1

Same as page 1

RAW SEQUENCE LISTING DATE: 01/22/2003
PATENT APPLICATION: US/09/914,006C TIME: 13:42:48

Input Set : A:\SN09914006.asc
Output Set: N:\CRF4\01222003\I914006C.raw

Same as page 1

E--> 520 Leu
E--> 521 35 40 45
524 Leu Val Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr
E--> 525 Thr
E--> 526 50 55 60
529 Leu Ser Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val
E--> 530 Thr
E--> 531 65 70 75 80
534 Ile Ala Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly
E--> 535 Thr
E--> 536 85 90 95
539 Tyr Glu Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val
E--> 540 Met
E--> 541 100 105 110
544 Arg Glu Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu
E--> 545 Ile
E--> 546 115 120 125
549 Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val
E--> 550 Gly
E--> 551 130 135 140
554 His Ile Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His
E--> 555 Val
E--> 556 145 150 155
E--> 557 160
560 Val Gln Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala
E--> 561 Arg
E--> 562 165 170 175
565 Ala Leu Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val
E--> 566 Pro
E--> 567 180 185 190
570 Ala Glu Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr
E--> 571 Ile
E--> 572 195 200 205
575 Gly Ile Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp
E--> 576 Gln
E--> 577 210 215 220
580 Asp Ala Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg
E--> 581 Glu
E--> 582 225 230 235
E--> 583 240
586 Tyr Ala Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr
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E--> 588 245 250 255
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595 <210> SEQ ID NO: 5
596 <211> LENGTH: 279
597 <212> TYPE: PRT
598 <213> ORGANISM: Corynebacterium glutamicum

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Input Set : **A:\SN09914006.asc**
Output Set: **N:\CRF4\01222003\I914006C.raw**

600 <400> SEQUENCE: 5

```
602 Met Gln Val Ala Thr Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu
E--> 603 His
E--> 604 1                  5                  10                  15
607 His Lys Ser Val Gly Leu Val Pro Thr Met Gly Ala Leu His Ser
E--> 608 Gly
E--> 609                20                  25                  30
612 His Ala Ser Leu Val Lys Ala Ala Arg Ala Glu Asn Asp Thr Val
E--> 613 Val
E--> 614        35                  40                  45
617 Ala Ser Ile Phe Val Asn Pro Leu Gln Phe Glu Ala Leu Gly Asp
E--> 618 Cys
E--> 619    50                  55                  60
622 Asp Asp Tyr Arg Asn Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala
E--> 623 Leu
E--> 624 65                  70                  75                  80
627 Leu Glu Glu Ala Gly Val Asp Ile Val Phe Ala Pro Asp Val Glu
E--> 628 Glu
E--> 629                85                  90                  95
632 Met Tyr Pro Gly Gly Leu Pro Leu Val Trp Ala Arg Thr Gly Ser
E--> 633 Ile
E--> 634                100                 105                 110
637 Gly Thr Lys Leu Glu Gly Ala Ser Arg Pro Gly His Phe Asp Gly
E--> 638 Val
E--> 639        115                 120                 125
642 Ala Thr Val Val Ala Lys Leu Phe Asn Leu Val Arg Pro Asp Arg
E--> 643 Ala
E--> 644    130                 135                 140
647 Tyr Phe Gly Gln Lys Asp Ala Gln Gln Val Ala Val Ile Arg Arg
E--> 648 Leu
E--> 649 145                 150                 155
E--> 650 160
653 Val Ala Asp Leu Asp Ile Pro Val Glu Ile Arg Pro Val Pro Ile
E--> 654 Ile
E--> 655                165                 170                 175
658 Arg Gly Ala Asp Gly Leu Ala Glu Ser Ser Arg Asn Gln Arg Leu
E--> 659 Ser
E--> 660                180                 185                 190
663 Ala Asp Gln Arg Ala Gln Ala Leu Val Leu Pro Gln Val Leu Ser
E--> 664 Gly
E--> 665        195                 200                 205
668 Leu Gln Arg Arg Lys Ala Ala Gly Glu Ala Leu Asp Ile Gln Gly
E--> 669 Ala
E--> 670    210                 215                 220
673 Arg Asp Thr Leu Ala Ser Ala Asp Gly Val Arg Leu Asp His Leu
E--> 674 Glu
E--> 675 225                 230                 235
E--> 676 240
679 Ile Val Asp Pro Ala Thr Leu Glu Pro Leu Glu Ile Asp Gly Leu
```

RAW SEQUENCE LISTING DATE: 01/22/2003
PATENT APPLICATION: US/09/914,006C TIME: 13:42:48

Input Set : A:\SN09914006.asc
Output Set: N:\CRF4\01222003\I914006C.raw

E--> 680 Leu
E--> 681 245 250 255
684 Thr Gln Pro Ala Leu Val Val Gly Ala Ile Phe Val Gly Pro Val
E--> 685 Arg
E--> 686 260 265 270
689 Leu Ile Asp Asn Ile Glu Leu
E--> 690 275
693 <210> SEQ ID NO: 6
694 <211> LENGTH: 26
695 <212> TYPE: DNA
696 <213> ORGANISM: Corynebacterium glutamicum
698 <400> SEQUENCE: 6
E--> 699 gagaacttaa tcgagcaaca cccctg
700 26
703 <210> SEQ ID NO: 7
704 <211> LENGTH: 26
705 <212> TYPE: DNA
706 <213> ORGANISM: Corynebacterium glutamicum
708 <400> SEQUENCE: 7
E--> 709 gcgccacgcc tagccttggc cctcaa
710 26

VERIFICATION SUMMARY DATE: 01/22/2003
PATENT APPLICATION: **US/09/914,006C** TIME: 13:42:49

Input Set : **A:\SN09914006.asc**
Output Set: **N:\CRF4\01222003\I914006C.raw**

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:26 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:1
M:254 Repeated in SeqNo=1
L:185 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:390 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:3
M:254 Repeated in SeqNo=3
L:510 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
M:332 Repeated in SeqNo=4
L:603 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
M:332 Repeated in SeqNo=5
L:699 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:6
L:709 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:7